#9

OIPE

RAW SEQUENCE LISTING   DATE: 08/28/2001
PATENT APPLICATION: US/09/810,506   TIME: 09:53:58

Input Set : A:\204936US0.txt
Output Set: N:\CRF3\08282001\I810506.raw

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 3  <110> APPLICANT: TAJI, Teruaki
 4         SHINOZAKI, Kazuo
 5         OHSUMI, Chieko
 7  <120> TITLE OF INVENTION: A METHOD FOR INCREASING STRESS-RESISTANCE TO A PLANT
 9  <130> FILE REFERENCE: 20436US0
11  <140> CURRENT APPLICATION NUMBER: 09/810,506
12  <141> CURRENT FILING DATE: 2001-03-19
14  <150> PRIOR APPLICATION NUMBER: JP2001-072650
15  <151> PRIOR FILING DATE: 2001-03-14
17  <160> NUMBER OF SEQ ID NOS: 15
19  <170> SOFTWARE: PatentIn version 3.1
21  <210> SEQ ID NO: 1
22  <211> LENGTH: 344
23  <212> TYPE: PRT
24  <213> ORGANISM: Arabidopsis thaliana
26  <400> SEQUENCE: 1
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33              20                  25                  30
36  Val Thr Phe Leu Ala Gly Asn Gly Asp Tyr Val Lys Gly Val Val Gly
37          35                  40                  45
40  Leu Ala Lys Gly Leu Arg Lys Val Lys Ser Ala Tyr Pro Leu Val Val
41      50                  55                  60
44  Ala Met Leu Pro Asp Val Pro Glu Glu His Arg Arg Ile Leu Val Asp
45  65                  70                  75                  80
48  Gln Gly Cys Ile Val Arg Glu Ile Glu Pro Val Tyr Pro Pro Glu Asn
49              85                  90                  95
52  Gln Thr Gln Phe Ala Met Ala Tyr Tyr Val Ile Asn Tyr Ser Lys Leu
53              100                 105                 110
56  Arg Ile Trp Lys Phe Val Glu Tyr Ser Lys Met Ile Tyr Leu Asp Gly
57          115                 120                 125
60  Asp Ile Gln Val Tyr Glu Asn Ile Asp His Leu Phe Asp Leu Pro Asp
61      130                 135                 140
64  Gly Tyr Leu Tyr Ala Val Met Asp Cys Phe Cys Glu Lys Thr Trp Ser
65  145                 150                 155                 160
68  His Thr Pro Gln Tyr Lys Ile Arg Tyr Cys Gln Gln Cys Pro Asp Lys
69                  165                 170                 175
72  Val Gln Trp Pro Lys Ala Glu Leu Gly Glu Pro Pro Ala Leu Tyr Phe
73              180                 185                 190
76  Asn Ala Gly Met Phe Leu Tyr Glu Pro Asn Leu Glu Thr Tyr Glu Asp
77          195                 200                 205
80  Leu Leu Arg Thr Leu Lys Ile Thr Pro Pro Thr Pro Phe Ala Glu Gln
81      210                 215                 220
84  Asp Phe Leu Asn Met Tyr Phe Lys Lys Ile Tyr Lys Pro Ile Pro Leu
85  225                 230                 235                 240
88  Val Tyr Asn Leu Val Leu Ala Met Leu Trp Arg His Pro Glu Asn Val
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89                    245                   250                   255
92 Glu Leu Gly Lys Val Lys Val Val His Tyr Cys Ala Ala Gly Ser Lys
93                    260                   265                   270
96 Pro Trp Arg Tyr Thr Gly Lys Glu Ala Asn Met Glu Arg Glu Asp Ile
97             275                   280                   285
100 Lys Met Leu Val Lys Lys Trp Trp Asp Ile Tyr Asp Asp Glu Ser Leu
101          290                   295                   300
104 Asp Tyr Lys Lys Pro Val Thr Val Val Asp Thr Glu Val Asp Leu Val
105 305                   310                   315                   320
108 Asn Leu Lys Pro Phe Ile Thr Ala Leu Thr Glu Ala Gly Arg Leu Asn
109             325                   330                   335
112 Tyr Val Thr Ala Pro Ser Ala Ala
113             340
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117 <211> LENGTH: 335
118 <212> TYPE: PRT
119 <213> ORGANISM: Arabidopsis thaliana
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127 Thr Gly Gly Glu Lys Arg Ala Tyr Val Thr Phe Leu Ala Gly Thr Gly
128             20                    25                    30
131 Asp Tyr Val Lys Gly Val Val Gly Leu Ala Lys Gly Leu Arg Lys Ala
132          35                    40                    45
135 Lys Ser Lys Tyr Pro Leu Val Val Ala Val Leu Pro Asp Val Pro Glu
136     50                    55                    60
139 Asp His Arg Lys Gln Leu Val Asp Gln Gly Cys Val Val Lys Glu Ile
140 65                    70                    75                    80
143 Glu Pro Val Tyr Pro Pro Glu Asn Gln Thr Glu Phe Ala Met Ala Tyr
144                   85                    90                    95
147 Tyr Val Ile Asn Tyr Ser Lys Leu Arg Ile Trp Glu Phe Val Glu Tyr
148             100                   105                   110
151 Asn Lys Met Ile Tyr Leu Asp Gly Asp Ile Gln Val Phe Asp Asn Ile
152          115                   120                   125
155 Asp His Leu Phe Asp Leu Pro Asn Gly Gln Phe Tyr Ala Val Met Asp
156     130                   135                   140
159 Cys Phe Cys Glu Lys Thr Trp Ser His Ser Pro Gln Tyr Lys Ile Gly
160 145                   150                   155                   160
163 Tyr Cys Gln Gln Cys Pro Asp Lys Val Thr Trp Pro Glu Ala Lys Leu
164             165                   170                   175
167 Gly Pro Lys Pro Pro Leu Tyr Phe Asn Ala Gly Met Phe Val Tyr Glu
168             180                   185                   190
171 Pro Asn Leu Ser Thr Tyr His Asn Leu Leu Glu Thr Val Lys Ile Val
172          195                   200                   205
175 Pro Pro Thr Leu Phe Ala Glu Gln Asp Phe Leu Asn Met Tyr Phe Lys
176 210                   215                   220
179 Asp Ile Tyr Lys Pro Ile Pro Pro Val Tyr Asn Leu Val Leu Ala Met
180 225                   230                   235                   240
183 Leu Trp Arg His Pro Glu Asn Ile Glu Leu Asp Gln Val Lys Val Val
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184                245                 250                  255
187 His Tyr Cys Ala Ala Gly Ala Lys Pro Trp Arg Phe Thr Gly Glu Glu
188              260                 265                  270
191 Glu Asn Met Asp Arg Glu Asp Ile Lys Met Leu Val Lys Lys Trp Trp
192              275                 280                  285
195 Asp Ile Tyr Asn Asp Glu Ser Leu Asp Tyr Lys Asn Val Val Ile Gly
196         290                 295                  300
199 Asp Ser His Lys Lys Gln Gln Thr Leu Gln Gln Phe Ile Glu Ala Leu
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215 tcactgccat cagtccaaga cagcgatcga gcttacgtga cgtttcttgc tggaaacggt   120
217 gattacgtga aaggagtcgt tggtttagcc aaagggttaa ggaaagtcaa atcggcttat   180
219 ccactcgtag tagcgatgtt acccgacgtc ccggaggaac accgtcgtat acttgtggat   240
221 caaggatgca tcgtccgtga aatcgaaccc gtttacccac ccgagaacca aactcagttc   300
223 gccatggctt attacgtcat caactactct aaactccgta tctggaagtt tgtggagtat   360
225 agtaaaatga tatatttaga tggagacatt caagtttacg aaaacatcga tcacttgttt   420
227 gacctaccag atggctattt gtacgcggtg atggattgtt tctgtgagaa aacatggagt   480
229 cacacgccgc aatacaagat cagatattgc caacaatgcc ccgacaaagt ccagtggcca   540
231 aaagcggagc ttggagagcc accggctctt tacttcaacg ccggaatgtt cttgtacgag   600
233 cctaacctcg agacttacga ggatctacta cgaacactta aaatcactcc tccgactcct   660
235 ttcgctgaac aggatttttt gaacatgtac tttaagaaaa tctacaagcc gattccttta   720
237 gtgtacaatc tcgtccttgc gatgttatgg cgtcacccag aaaatgtaga gcttggaaaa   780
239 gtcaaggtgg ttcactactg tgcagcgggt tcgaagccgt ggagatacac agggaaagaa   840
241 gcgaacatgg agagggaaga tataaaaatg ttagtgaaaa aatggtggga catttacgac   900
243 gacgaatcct tggattacaa gaaacctgtt accgttgtgg acacagaggt cgatctcgtg   960
245 aatctgaagc cgttcatcac cgctcttact gaagctggcc ggctcaacta cgtgaccgca  1020
247 ccgtccgctg cttgaatgtt gccaggagtt aaaattgtcg gtgg                   1064
250 <210> SEQ ID NO: 4
251 <211> LENGTH: 29
252 <212> TYPE: DNA
253 <213> ORGANISM: Artificial Sequence
255 <220> FEATURE:
256 <223> OTHER INFORMATION: synthetic DNA
258 <400> SEQUENCE: 4
259 caaggatccg cagatcacgt gctaatcac                                       29
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263 <211> LENGTH: 29
264 <212> TYPE: DNA
265 <213> ORGANISM: Artificial Sequence
267 <220> FEATURE:
268 <223> OTHER INFORMATION: synthetic DNA
270 <400> SEQUENCE: 5
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271 caaggatccc ctggcaatca agcagcgga                          29
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276 <212> TYPE: DNA
277 <213> ORGANISM: Artificial Sequence
279 <220> FEATURE:
280 <223> OTHER INFORMATION: synthetic DNA
282 <400> SEQUENCE: 6
283 cgccacagta caagatcggt ta                                  22
286 <210> SEQ ID NO: 7
287 <211> LENGTH: 20
288 <212> TYPE: DNA
289 <213> ORGANISM: Artificial Sequence
291 <220> FEATURE:
292 <223> OTHER INFORMATION: synthetic DNA
294 <400> SEQUENCE: 7
295 catgaagagg cgtatgcagc                                     20
298 <210> SEQ ID NO: 8
299 <211> LENGTH: 20
300 <212> TYPE: DNA
301 <213> ORGANISM: Artificial Sequence
303 <220> FEATURE:
304 <223> OTHER INFORMATION: synthetic DNA
306 <400> SEQUENCE: 8
307 ctttctcgga caagatggca                                     20
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311 <211> LENGTH: 20
312 <212> TYPE: DNA
313 <213> ORGANISM: Artificial Sequence
315 <220> FEATURE:
316 <223> OTHER INFORMATION: synthetic DNA
318 <400> SEQUENCE: 9
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323 <211> LENGTH: 32
324 <212> TYPE: DNA
325 <213> ORGANISM: Artificial Sequence
327 <220> FEATURE:
328 <223> OTHER INFORMATION: synthetic DNA
330 <400> SEQUENCE: 10
331 cgcggatcca tggctccggg gcttactcaa ac                       32
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335 <211> LENGTH: 32
336 <212> TYPE: DNA
337 <213> ORGANISM: Artificial Sequence
339 <220> FEATURE:
340 <223> OTHER INFORMATION: synthetic DNA
342 <400> SEQUENCE: 11
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346 <210> SEQ ID NO: 12
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352 <223> OTHER INFORMATION: synthetic DNA
354 <400> SEQUENCE: 12
355 cgcggatcca tggcacctga gatcaatacc                              30
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359 <211> LENGTH: 30
360 <212> TYPE: DNA
361 <213> ORGANISM: Artificial Sequence
363 <220> FEATURE:
364 <223> OTHER INFORMATION: synthetic DNA
366 <400> SEQUENCE: 13
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371 <211> LENGTH: 36
372 <212> TYPE: DNA
373 <213> ORGANISM: Artificial Sequence
375 <220> FEATURE:
376 <223> OTHER INFORMATION: synthetic DNA
378 <400> SEQUENCE: 14
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385 <213> ORGANISM: Artificial Sequence
387 <220> FEATURE:
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390 <400> SEQUENCE: 15
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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/810,506

DATE: 08/28/2001
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